

X GGG ||| GGG

2. US 08-973-363-1 (1-723)
US 08-973-363-15 Sequence 15, Application US/08973363-15

Initial Score	=	62	Optimized Score	=	169	Signi
Residue Identity	=	328	Matches	=	174	Misma
Alphaps	=	3	Conservative Substitutions			

TGTAAATTATTCTGATCTTGTAGCGAAGTTGTTGGGATTTAGTTGGTTCCCTGTACTGT
140 150 160 170 180 X 190 200

ALLIANCE FOR CHILDREN
X 10 20

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GATCATAGAAAGAATATCTGAAAGGCCAAGAAAAAGCTTAGACATTTAGTGATTGAGAGA
30
30
280 290 300 310 320 330 340
280 290 300 310 320 330 340

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3550	360	100	110	120	130	140	150	160	420
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AGGAGATGGATATAGATGAATCTTGAAGGGNCTGAAACTCAGGAGAATTCAGGCCATTAATGTTAG
240
250 260 270 280 290 300 310

500 510 520 530 540 550 560
ATGAGTTAATGCAATTAGAACCATGGCAGAACATTAGGAGATCTGTGGATGACAGTGTACAGGAGTCGTGA

GAGATGAGTTACTTTCACAGTTCAAGGTAGCTAACTTTCCAAATGAGATGAACTGGAA - -TTGG
320 330 340 350 360 370

ATTTTTAGATAACTGAGTGGAAACAGAAATCTGGGCTAGTTCTGAGCTGACTTAAATTGTTG
570 580 590 600 610 620 630

GAGATATTCGAACTCATTTGTTGAGAAATAATGTTAGTTGTCATCCTTGA
AAAGAAAAAGAACTTGGAAATAATATGCTCCAGAATGAGAACATGGCA
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710 460 470 480 490 500 510 520
720 X

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      AACCTCCGACGGG
      ||| | |
ATGGAAATGGAAAGGGCTAGTGGAGGCGAGAAGATATTCTGGATCTGATAGTGTCTCA
  5'30 540 550 560 570 580

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0 <
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 stDB - Fast Pairwise Comparison of Sequences
 Please 5.4

Results file seq10-seqland15.res made by mruhl on Thu 22 May 103 10:36:55-PM

every sequence being compared: US-08-973-363-10 (1-6608)
 number of sequences searched: 18
 number of scores above cutoff: 18

Results of the initial comparison of US-08-973-363-10 (1-6608) with:
 File : US08973363.seq

Score Range	Frequency
0-1467	734
1468-2202	1468
2203-3670	2203
3671-4405	2937
4406-5140	2
5141-5874	3671
5875-6608	4

PARAMETERS	4	30	500
similarity matrix	Unitary	K-tuple	
ismatch penalty	1	Joining penalty	
o penalty	5.00	Window size	

penalty score combination 0.33 1 2

SEARCH STATISTICS

Mean Median Standard Deviation
scores : 100 100 100

• $\frac{1}{2}$ $\frac{1}{3}$ $\frac{1}{4}$ $\frac{1}{5}$ $\frac{1}{6}$ $\frac{1}{7}$ $\frac{1}{8}$ $\frac{1}{9}$ $\frac{1}{10}$ $\frac{1}{11}$ $\frac{1}{12}$ $\frac{1}{13}$ $\frac{1}{14}$ $\frac{1}{15}$ $\frac{1}{16}$ $\frac{1}{17}$ $\frac{1}{18}$ $\frac{1}{19}$ $\frac{1}{20}$ $\frac{1}{21}$ $\frac{1}{22}$ $\frac{1}{23}$ $\frac{1}{24}$ $\frac{1}{25}$ $\frac{1}{26}$ $\frac{1}{27}$ $\frac{1}{28}$ $\frac{1}{29}$ $\frac{1}{30}$ $\frac{1}{31}$ $\frac{1}{32}$ $\frac{1}{33}$ $\frac{1}{34}$ $\frac{1}{35}$ $\frac{1}{36}$ $\frac{1}{37}$ $\frac{1}{38}$ $\frac{1}{39}$ $\frac{1}{40}$ $\frac{1}{41}$ $\frac{1}{42}$ $\frac{1}{43}$ $\frac{1}{44}$ $\frac{1}{45}$ $\frac{1}{46}$ $\frac{1}{47}$ $\frac{1}{48}$ $\frac{1}{49}$ $\frac{1}{50}$ $\frac{1}{51}$ $\frac{1}{52}$ $\frac{1}{53}$ $\frac{1}{54}$ $\frac{1}{55}$ $\frac{1}{56}$ $\frac{1}{57}$ $\frac{1}{58}$ $\frac{1}{59}$ $\frac{1}{60}$ $\frac{1}{61}$ $\frac{1}{62}$ $\frac{1}{63}$ $\frac{1}{64}$ $\frac{1}{65}$ $\frac{1}{66}$ $\frac{1}{67}$ $\frac{1}{68}$ $\frac{1}{69}$ $\frac{1}{70}$ $\frac{1}{71}$ $\frac{1}{72}$ $\frac{1}{73}$ $\frac{1}{74}$ $\frac{1}{75}$ $\frac{1}{76}$ $\frac{1}{77}$ $\frac{1}{78}$ $\frac{1}{79}$ $\frac{1}{80}$ $\frac{1}{81}$ $\frac{1}{82}$ $\frac{1}{83}$ $\frac{1}{84}$ $\frac{1}{85}$ $\frac{1}{86}$ $\frac{1}{87}$ $\frac{1}{88}$ $\frac{1}{89}$ $\frac{1}{90}$ $\frac{1}{91}$ $\frac{1}{92}$ $\frac{1}{93}$ $\frac{1}{94}$ $\frac{1}{95}$ $\frac{1}{96}$ $\frac{1}{97}$ $\frac{1}{98}$ $\frac{1}{99}$ $\frac{1}{100}$

Number of residues: 10306

The scores below are sorted by initial score.

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ללאו יתחייב בדין רשותו שאמור הוא כי מינהו מנהל יסודו של מושב:

Sequence Name	Description	Length	Init.	Opt.	Sig.	Frame
1. US-08-973-363-10	Sequence 10, Application	6608	6608	6608	3.95	0
2. US-08-973-363-15	Sequence 15, Application	1316	1176	1179	0.44	0
3. US-08-973-363-32	Sequence 32, Application	111	111	111	-0.25	0
4. US-08-973-363-3	Sequence 3, Application US	153	103	115	-0.25	0
5. US-08-973-363-4	Sequence 34, Application	111	101	101	-0.26	0
6. US-08-973-363-16	Sequence 36, Application	111	99	99	-0.26	0
7. US-08-973-363-4	Sequence 4, Application US	153	98	111	-0.26	0
8. US-08-973-363-5	Sequence 5, Application US	153	94	107	-0.26	0
9. US-08-973-363-2	Sequence 2, Application US	153	94	96	-0.26	0
10. US-08-973-363-12	Sequence 12, Application	265	94	115	-0.26	0
11. US-08-973-363-31	Sequence 31, Application	111	91	94	-0.26	0
12. US-08-973-363-33	Sequence 33, Application	117	61	61	-0.28	0
13. US-08-973-363-35	Sequence 35, Application	67	59	59	-0.28	0
14. US-08-973-363-1	Sequence 1, Application US	723	49	252	-0.29	0
1. US-08-973-363-10	(1-6608)					
US-08-973-363-10	Sequence 10, Application	6608	6608	6608	3.95	0
Initial Score	Optimized Score	-	6608	Significance	=	3.95
Residue Identity	Matches	-	6608	Mismatches	-	0
Gaps	0	0	0	0	0	0
X	10	20	30	40	50	60
	CGGGCTGCACGACGCAACGGCACCGCCGCGCCAGCGAGGTGGCCGGGAAAGGCCCTGGCCGACGGCG					
X	10	20	30	40	50	60
	CGGGCTGCACGACGCAACGGCACCGCCGCGCCAGCGAGGTGGCCGGGAAAGGCCCTGGCCGACGGCG					
X	10	20	30	40	50	60
	ACCGAGGTGGTATTGGCAAAATCTGGCCATCTGGCAAACTGGCAAGTCAAGCGATTACTTCGAAA					
80	90	100	110	120	130	140
	ACCGAGGTGGTATTGGCAAAATCTGGCAAACTGGCAAGTCAAGCGATTACTTCGAAA					
80	90	100	110	120	130	140

ACATAGGAGTACCAAGAAAGGGATTCTTGACCTCACCTGAAACCTGAGTGACTCTTAACTCT
 ACATAGGAGTACCAAGAAAGGGATTCTTGACCTCACCTGAAACCTGAGTGACTCTTAACTCT
 150 160 170 180 190- 200 210
 220 230 240 250 260 270 280
 TAATACTACATGAACTGAGTGTGAGTAAACAGGAGTGGAGACGACAGATCAG
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 TAATACTACATGAACTGAGTGTGAGTGTAAAGCTGAGTAAACAGGAGTGGAGACGACAG
 220 230 240 250 260 270 280
 290 300 310 320 330 340 350 360
 ATGATGATCTGGCTACGTCAGTTGGATCTGGTCAAGCTCTGGAAAGCAGTGGAGTGGAG
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 ATGATGATCTGGCTACGTCAGTTGGATCTGGTCAAGCTCTGGAAAGCAGTGGAGTGGAG
 290 300 310 320 330 340 350 360
 370 380 390 400 410 420 430
 GCGAGTCAGTAGCTTACGTTGACTCTGAACTCTGGTCAAGCTGAGCTCACTATCCGAAT
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 GCGAGTCAGTAGCTTACGTTGACTCTGAACTCTGGTCAAGCTGAGCTCACTATCCGAAT
 370 380 390 400 410 420 430
 440 450 460 470 480 490 500
 CTAGAGAGAAAACAGTCAACGCTAAACCTCCAAAAGCTGAGCTGAGTGTGAGTGGAGT
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 CTAGAGAGAAAACAGTCAACGCTAAACCTCCAAAAGCTGAGCTGAGTGTGAGTGGAGT
 440 450 460 470 480 490 500
 510 520 530 540 550 560 570

580 590 600 610 620 630 640
 GTGGTTCAGAAGAGGACTCATCCAGTAGTGAAGATTCTGGGATGATTCGCCCCACTGAACTAAGAGAAAA
 GTGGTTCAGAAGGACTCATCCAGTAGTGAAGATTCTGGGATGATTCGCCCCACTGAACTAAGAGAAAA
 580 590 600 610 620 630 640
 580 590 600 610 620 630 640
 AGCATTAAGATGAAGACTGCCCCAAATGTCAGGGTCAGGTCAGGAACTGTTCTGATGAACTGGGATGATTCG
 AGCATTAAGATGAAGACTGCCCCAAATGTCAGGGTCAGGTCAGGAACTGTTCTGATGAACTGGGATGATTCG
 650 660 670 680 690 700 710 720
 CCGGAGATGGGATAAAAGCAGTCTGAAAGTGTACTGATGAGGAACTGTTCTGATGAACTGGGATGATTCG
 CCGGAGATGGGATAAAAGCAGTCTGAAAGTGTACTGATGAGGAACTGTTCTGATGAACTGGGATGATTCG
 730 740 750 760 770 780 790 800
 GTAAACCTCCAAGCAGATAAAGCCAAAATGTCAGGGACAGGACAGGACAGAGAAGGCAACTGTATT
 GTAAACCTCCAAGCAGATAAAGCCAAAATGTCAGGGACAGGACAGGACAGAGAAGGCAACTGTATT
 800 810 820 830 840 850 860
 CATCAGGGAGGAGGAGCATGATGAAAGTATGATAAGAGGATCTGTCGCAAGGAAACAGTGAATG
 CATCAGGGAGGAGGAGCATGATGAAAGTATGATAAGAGGATCTGTCGCAAGGAAACAGTGAATG
 870 880 890 900 910 920 930
 TTAGTTACAAAGAAGCTGCTGAAAACCAAGACAGATTCCTGATGATTCTGCTGAAAGTGTGAGAGGATG
 TTAGTTACAAAGAAGCTGCTGAAAACCAAGACAGATTCCTGATGATTCTGCTGAAAGTGTGAGAGGATG
 940 950 960 970 980 990 1000
 CACAGACTGAGAAGTGAACCATATGAGCAAGTGTGAGAGGATG
 CACAGACTGAGAAGTGAACCATATGAGCAAGTGTGAGAGGATG
 940 950 960 970 980 990 1000
 TTAGTTACAAAGAAGCTGCTGAAAACCAAGACAGATTCCTGATGATTCTGCTGAAAGTGTGAGAGGATG
 TTAGTTACAAAGAAGCTGCTGAAAACCAAGACAGATTCCTGATGATTCTGCTGAAAGTGTGAGAGGATG
 940 950 960 970 980 990 1000
 CACAGACTGAGAAGTGAACCATATGAGCAAGTGTGAGAGGATG
 CACAGACTGAGAAGTGAACCATATGAGCAAGTGTGAGAGGATG
 1010 1020 1030 1040 1050 1060 1070 1080
 CTCGGTCCTCAACCCACATCTATGGCACAGTTATGGCACAGTCGAATGGCCGAAAGGAGCA
 CTCGGTCCTCAACCCACATCTATGGCACAGTTATGGCACAGTCGAATGGCCGAAAGGAGCA
 1010 1020 1030 1040 1050 1060 1070 1080
 1160 1170 1180 1190 1200 1210 1220 1230
 AGCAGGGAGAAATACAGTATCTTAAATGGAAGGGCTGGTCACACATCCATACACAGTCGAAG
 AGCAGGGAGAAATACAGTATCTTAAATGGAAGGGCTGGTCACACATCCATACACAGTCGAAG
 1160 1170 1180 1190 1200 1210 1220 1230
 AACCGCTGAGCAACAAATGCTTCAGAACATGCAACTACAAGGAAAGGATCAGGAGACAA
 AACCGCTGAGCAACAAATGCTTCAGAACATGCAACTACAAGGAAAGGATCAGGAGACAA
 1300 1310 1320 1330 1340 1350 1360
 AACCGCTGAGCAACAAATGCTTCAGAACATGCAACTACAAGGAAAGGATCAGGAGACAA
 AACCGCTGAGCAACAAATGCTTCAGAACATGCAACTACAAGGAAAGGATCAGGAGACAA
 1300 1310 1320 1330 1340 1350 1360
 TGCACAAACATTCATGCTTCAGAACATGCAACTACAAGGAAAGGATCAGGAGACAA
 TGCACAAACATTCATGCTTCAGAACATGCAACTACAAGGAAAGGATCAGGAGACAA
 1370 1380 1390 1400 1410 1420 1430 1440

2240 2250 2260 2270 2280 2290 2300
 2310 2320 2330 2340 2350 2360 2370
 GAAGACTTAAAGATGTAGAAAGCTTTACCTGCTTAAGGTGAAATTCCTAGGTGAAATGACTG
 GAAGCTTAAAGATGTAGAAAGCTTTACCTGCTTAAGGTGAAATGACTG
 2310 2320 2330 2340 2350 2360 2370
 2380 2390 2400 2410 2420 2430 2440
 CATTGAGAAAGATAATTACAACTGGATTAAAGAAATTAAGGCCCTAACGTTCAAGGTCAAAGGCC
 CATTGAGAAAGATAATTACAACTGGATTAAAGAAATTAAGGCCCTAACGTTCAAGGTCAAAGGCC
 2380 2390 2400 2410 2420 2430 2440
 2450 2460 2470 2480 2490 2500 2510
 GTACCTCAGCTTCGAGCATPATGTTGAACTTAAGAAGCTTGTAACCTTGTAACTCTTAACTGCC
 GTACCTCAGCTTCGAGCATPATGTTGAACTTAAGAAGCTTGTAACCTTGTAACTCTTAACTGCC
 2450 2460 2470 2480 2490 2500 2510
 2510 2520 2530 2540 2550 2560 2570
 CAGATGATATGAATTCTATATAAACGGGCTTACAGATTGAACTGTTGAACTGAACTTAACTCC
 CAGATGATATGAATTCTATATAAACGGGCTTACAGATTGAACTGTTGAACTGAACTTAACTCC
 2510 2520 2530 2540 2550 2560 2570
 2600 2610 2620 2630 2640 2650 2660
 TCTTGACAGCTACGATCTGCTGAGACCTGGAAACAGGCTTGATGTTCTCAGTTGAGGAGA
 TCTTGACAGCTACGATCTGCTGAGACCTGGAAACAGGCTTGATGTTCTCAGTTGAGGAGA
 2600 2610 2620 2630 2640 2650 2660
 2670 2680 2690 2700 2710 2720 2730
 TGCTGGACATCTTACGAGAATATGTAAAGTTGAACTGTTGAGCTAAAG
 TGCTGGACATCTTACGAGAATATGTAAAGTTGAACTGTTGAGCTAAAG
 2670 2680 2690 2700 2710 2720 2730
 2740 2750 2760 2770 2780 2790 2800
 GGGATTGAGGAAAGCACTGGATCATTCATGCAAGAAGCTGAGGATTCTGTTTACTGCTTA
 GGGATTGAGGAAAGCACTGGATCATTCATGCAAGAAGCTGAGGATTCTGTTTACTGCTTA
 2740 2750 2760 2770 2780 2790 2800
 2810 2820 2830 2840 2850 2860 2870 2880
 CAAGACCTGGACCTTAACTGCTGATCTGCTGAACTTGTGTTTACTGCTTA
 CAAGACCTGGACCTTAACTGCTGATCTGCTGAACTTGTGTTTACTGCTTA
 2810 2820 2830 2840 2850 2860 2870 2880
 2890 2900 2910 2920 2930 2940 2950
 CACAGAATTCCTGGAGCAAGGCAAGCTCATAGAATGGAGAACAGCTTAACTTCG
 CACAGAATTCCTGGAGCAAGGCAAGCTCATAGAATGGAGAACAGCTTAACTTCG
 2890 2900 2910 2920 2930 2940 2950
 2960 2970 2980 2990 3000 3010 3020
 TAGTCACAAAGGATCTGAGAACGATATTTCTGAAAGGAAAGCTTACGTTAACTTCG
 TAGTCACAAAGGATCTGAGAACGATATTTCTGAAAGGAAAGCTTACGTTAACTTCG
 2960 2970 2980 2990 3000 3010 3020
 3030 3040 3050 3060 3070 3080 3090
 TAATTCAGAAATGGAGAACGACCAAGGAAAGCTTACGTTAACTTCG
 TAATTCAGAAATGGAGAACGACCAAGGAAAGCTTACGTTAACTTCG
 3030 3040 3050 3060 3070 3080 3090
 3100 3110 3120 3130 3140 3150 3160
 TAATTAAGAAGAGTTATGCTTATTTGAGTTGGCTTAAGGAACTGTTGAGGAG
 TAATTAAGAAGAGTTATGCTTATTTGAGTTGGCTTAAGGAACTGTTGAGGAG
 3110 3120 3130 3140 3150 3160 3170

Initial Score	Optimized Score	Residue Identity	Conservative Substitutions	Mismatches	Significance
5770 5780 5790 5800 5810 5820 5830	2970 2980 2990 3000 3010 3020 3030	GATCAGTAAAGAGATGGGGATTATTTCTCTTGTAGAAGACTCAGAGCTT	1176	89%	0.44
5840 5850 5860 5870 5880 5890 5900	2900 2910 2920 2930 2940 2950 2960	TGCAAGGAGGAGGTACAGTTAATGGACAGAAAGGTTAATGCTTATGCAAC	1179	89%	0.44
5910 5920 5930 5940 5950 5960 5970	2970 2980 2990 3000 3010 3020 3030	GATCAGTAAAGAGATGGGGATTATTTCTCTTGTAGAAGACTCAGAGCTT	1184	89%	0.44
5980 5990 6000 6010 6020 6030 6040	3040 3050 3060 3070 3080 3090 3100	TGGACACCGAGGAAACTGCTACTACAGCTCTTAAAGCTTAAAGGAGG	1185	89%	0.44
6050 6060 6070 6080 6090 6100 6110	3110 3120 3130 3140 3150 3160 3170	AGTTATCAGCTTAACTGCTTGTGGTAACTCTTAAAGGAGGAAAGAC	1186	89%	0.44
6130 6140 6150 6160 6170 6180 6190	3190 3200 3210 3220 3230 3240 3250	AGGAATGGATATAGTAATGAAATCTTGTAGGAGCTTAACTGGGAA	1187	89%	0.44
6200 6210 6220 6230 6240 6250 6260	3260 3270 3280 3290 3300 3310 3320	GGGATAGTGTGCTTCAGGCGGAACATTTCACATGGTAACTTGTGAA	1188	89%	0.44
6270 6280 6290 6300 6310 6320 6330	3330 3340 3350 3360 3370 3380 3390	CAGAAGAAATTAAAGGAATTCAGGCGGAACATTTCACATGGTAACTTGT	1189	89%	0.44
6340 6350 6360 6370 6380 6390 6400	3400 3410 3420 3430 3440 3450 3460	GCAAAAGAACCTGAGAAATAATACATGCTCCAGGGTAACTGTGAACT	1190	89%	0.44
6410 6420 6430 6440 6450 6460 6470	3470 3480 3490 3500 3510 3520 3530	GGAGTGAAGGAGCCAGTGGAGCAGAAAGATATTCTGATAGTGA	1191	89%	0.44
6560 6570 6580 6590 6600 6610 6620	3550 3560 3570 3580 3590 3600 3610	GGCCAAAAAAGGCTGGAGACCATCCCGAGAAATAATTAAAGGGATT	1192	89%	0.44
6690 6700 6710 6720 6730 6740 6750	3620 3630 3640 3650 3660 3670 3680	GCGGGTTATCAAGAGTAAAGAAATTGGCTGAGCTTAACTGAGAT	1193	89%	0.44
6760 6770 6780 6790 6800 6810 6820	3690 3700 3710 3720 3730 3740 3750	TGTCGATGATGAACTCTTGTGCTGAAAGTAACTTAACTGAACT	1194	89%	0.44

4. US-03-373-163-10 (1-608)
US-03-373-163-10
Sequence 1, Application US/0373163
Initial Identity = 49 Optimized Score = 252 Sign
Residue Identity = 38% Matches = 290 Misname
= 32 Conservative Substitutions
Aaps

1. US-08-973-363-10 (1-6608) US-08-973-363-1 Sequence 1, Application US/08973363	Initial Score = 94 Optimized Score = 107 Significance = -0.26 Residue Identity = 69% Matches = 107 Conservative Substitutions = 0 Gaps = 0	Residue Identity = 628 Matches = 0 Conservative Substitutions = 96 Mismatches = - 57 Gaps = 0
2. US-08-973-363-2 (1-6608) US-08-973-363-2 Sequence 2, Application US/08973363	Initial Score = 94 Optimized Score = 107 Significance = -0.26 Residue Identity = 69% Matches = 107 Conservative Substitutions = 94 Mismatches = - 17 Gaps = 0	Initial Score = 91 Optimized Score = 94 Significance = -0.26 Residue Identity = 84% Matches = 94 Conservative Substitutions = 94 Mismatches = - 0
3. US-08-973-363-3 (1-6608) US-08-973-363-3 Sequence 3, Application US/08973363	Initial Score = 94 Optimized Score = 107 Significance = -0.26 Residue Identity = 69% Matches = 107 Conservative Substitutions = 96 Mismatches = - 57 Gaps = 0	Initial Score = 91 Optimized Score = 94 Significance = -0.26 Residue Identity = 84% Matches = 94 Conservative Substitutions = 94 Mismatches = - 17 Gaps = 0
4. US-08-973-363-4 (1-6608) US-08-973-363-4 Sequence 4, Application US/08973363	Initial Score = 98 Optimized Score = 111 Significance = -0.26 Residue Identity = 73% Matches = 119 Conservative Substitutions = 34 Gaps = 9	Initial Score = 94 Optimized Score = 115 Significance = -0.26 Residue Identity = 45% Matches = 120 Conservative Substitutions = 120 Mismatches = - 144 Gaps = 1
5. US-08-973-363-5 (1-6608) US-08-973-363-5 Sequence 5, Application US/08973363	Initial Score = 94 Optimized Score = 107 Significance = -0.26 Residue Identity = 69% Matches = 107 Conservative Substitutions = 0 Gaps = 0	Initial Score = 94 Optimized Score = 115 Significance = -0.26 Residue Identity = 45% Matches = 120 Conservative Substitutions = 120 Mismatches = - 144 Gaps = 0
6. US-08-973-363-6 (1-6608) US-08-973-363-6 Sequence 6, Application US/08973363	Initial Score = 94 Optimized Score = 107 Significance = -0.26 Residue Identity = 69% Matches = 107 Conservative Substitutions = 0 Gaps = 0	Initial Score = 91 Optimized Score = 94 Significance = -0.26 Residue Identity = 84% Matches = 94 Conservative Substitutions = 94 Mismatches = - 17 Gaps = 0
7. US-08-973-363-10 (1-6608) US-08-973-363-1 Sequence 7, Application US/08973363	Initial Score = 98 Optimized Score = 111 Significance = -0.26 Residue Identity = 73% Matches = 119 Conservative Substitutions = 34 Gaps = 9	Initial Score = 94 Optimized Score = 115 Significance = -0.26 Residue Identity = 45% Matches = 120 Conservative Substitutions = 120 Mismatches = - 144 Gaps = 0
8. US-08-973-363-10 (1-6608) US-08-973-363-8 Sequence 8, Application US/08973363	Initial Score = 94 Optimized Score = 107 Significance = -0.26 Residue Identity = 69% Matches = 107 Conservative Substitutions = 0 Gaps = 0	Initial Score = 91 Optimized Score = 94 Significance = -0.26 Residue Identity = 84% Matches = 94 Conservative Substitutions = 94 Mismatches = - 17 Gaps = 0
9. US-08-973-363-10 (1-6608) US-08-973-363-2 Sequence 9, Application US/08973363	Initial Score = 94 Optimized Score = 96 Significance = -0.26 Residue Identity = 84% Matches = 94 Conservative Substitutions = 94 Mismatches = - 0	Initial Score = 91 Optimized Score = 94 Significance = -0.26 Residue Identity = 84% Matches = 94 Conservative Substitutions = 94 Mismatches = - 0
10. US-08-973-363-10 (1-6608) US-08-973-363-12 Sequence 12, Application US/08973363	Initial Score = 94 Optimized Score = 115 Significance = -0.26 Residue Identity = 45% Matches = 120 Conservative Substitutions = 120 Mismatches = - 144 Gaps = 0	Initial Score = 91 Optimized Score = 94 Significance = -0.26 Residue Identity = 84% Matches = 94 Conservative Substitutions = 94 Mismatches = - 17 Gaps = 0
11. US-08-973-363-10 (1-6608) US-08-973-363-31 Sequence 31, Application US/08973363	Initial Score = 91 Optimized Score = 94 Significance = -0.26 Residue Identity = 84% Matches = 94 Conservative Substitutions = 94 Mismatches = - 0	Initial Score = 91 Optimized Score = 94 Significance = -0.26 Residue Identity = 84% Matches = 94 Conservative Substitutions = 94 Mismatches = - 0

PARAMETER	UNITARY	K-1
Similarity matrix	1	JO
Mismatch penalty	5.00	WI
GAP Penalty	0.33	
GAP size penalty	1	
Cutoff score	0	
Randomization group		

	SEARCH S	MEAN
Scores:	Mean	32
Times:	CPU	

Number of residues: Number of sequences searched:
 Number of scores above cutoff: Number of sequences searched:

The scores below are sorted by initial significance is calculated based on a 100% identical sequence to the query.



5. US-08-973-363-10' (1-6608) US-08-973-363-12 Sequence 12, Application US/08973363	Initial Score = 40 Optimized Score = 102 Significance = 0.32 Residue Identity = 41% Matches = 120 Conservative Substitutions = 0 Gaps = 26	Initial Score = 31 Optimized Score = 49 Significance = -0.04 Residue Identity = 35% Matches = 55 Mismatches = 92 Gaps = 6
70 80 90 100 110 120 130 140 TAACATTCTGCTTAATAAAGTCATTCAAATCTCTAAATAACTGCTGATAGCACATTGACATT GATGAGATGTTCTAGTGAAC X 10 20	2970 2980 2990 3000 3010 3020 3030 CAAAATTCTCTGTAACTCTGATCTGATCACTAAATCTCTTAATATTTCAGGAA ATTATTACCTGATGATCCAGACA X 10 20	31 35%保守性Substitutions Gaps = 6
150 160 170 180 190 200 210 220 GCCCAAGTTAAAGGGAAACAAATGGATTACATGAACTGGCTGATCTGGGTTGAAAGTGTTCAC ATCTACATAAAAAAATAAACAGAAAAAAAGAAATGAAAGAACCTGAGCATATTG-----GTA 30 40 50 60 70 80 90 220 230 240 250 260 270 280 TATAGACACUTCCUTCTCTTAAACCAATTCAACCTGAAAAGCTTTCAGGGCACAGTTAGAGGGATATT TAAGAGGAAAGCTGAAGAAAAGAGACAAAAGAGAAAATAAAGGGATTCAGAACGG----- 90 100 110 120 130 140 150 290 300 310 320 330 340 350 CTCACTGTTCAATTACACATCACACACTGACAGTTAAATAGAAAAAAATAAAACACCAAA -----AGAAAAAGAAAAAGGAGGATANGAAAGAAATAAAGATATAAAGAAAGAG 160 170 180 190 200 210 360 370 380 390 400 410 420 ACAGGTATGAAAAGTATCCAAATAAAAGGACATAATGGATAAAATACTCCCTCCCATTTTACA AAAACAAAGTAAAGAAATCCACACAGAAAAGAAAGTGAAGGAAGAGAAG 220 230 240 250 260 X 430 440 450 460 TTCTGATTCCATCGAGATTTTATTAACAC 6. US-08-973-363-10' (1-6608) US-08-973-363-2 Sequence 2, Application US/08973363	2970 2980 2990 3000 3010 3020 3030 CAAAATTCTCTGTAACTCTGATCACTAAATCTCTTAATATTTCAGGAA ATTATTACCTGATGATCCAGACA X 10 20	31 35%保守性Substitutions Gaps = 6
3720 3730 3740 3750 3760 3770 3780 CCTGGAGATCAATTCTGGATTCTCAGTCAGAATCAAATAACTACAGTGTCAAGATGCCAAGTTATAC AAAACACAGCAAAACAGCTACAGACATAACAGCAAAACAGCAAAACAGTAAAGCCGTCAGACTAC 30 40 50 60 70 80 90 3790 3800 3810 3820 3830 3840 X 3850 CTAACATCCTCAGCTCTGTTAGACATTAACAGAAATCCTCTGATCCCTCTGATGAAATGATCCAGTG CTCATCAAAACTACTTGAGAGATCTGCAAGATGAAAGGGCTAGAAGCTTTCGGTCCG 100 110 120 130 140 150 X 3860 3870 3880 3890 CTTGCCTCCCAATTCCCTTTATTGATCCAGT 	3040 3050 3060 3070 3080 3090 3100 3110 TGGTTCGAGGTCTTCACCGTTTCTGCTGATGGAGTCACTATCAGATCCAGAATTC AGAAACCCAGCAAAGCAGCTACAGACCAAGAACCCAGGACATAGACCCGTTGCA 30 40 50 60 70 80 90 3120 3130 3140 3150 3160 X 3170 TTCTGCTCTTACTGGT-----CUTCCCTCACCTCCATTAAAGCTGTTGCA TCATAAAATTACTGATAAAAGACCTTGACAGAAAGAACGACAAAGGCTGCTG 100 110 120 130 140 150 X 3180 3190 3200 3210 TGGGAGCATGATATTTCTCAAGTTCTTGTCT 	31 35%保守性Substitutions Gaps = 6
8. US-08-973-363-10' (1-6608) US-08-973-363-4 Sequence 4, Application US/08973363	5770 5780 5790 5800 5810 5820 5830 5840 TGTGCTCTTTCCACTTTGGCTTAATCTGCTGGAGTTACGGCTTTGACTTGTGTTGGCT TCATAAAATTACTGATAAAAGACCTTGACAGAAAGAACGACTTGC 100 110 120 130 140 150 X 5990 6000 6010 6020 ATCATCGGCCAGAACCTCTCACTCTGGATGAGTCCTCT 	31 35%保守性Substitutions Gaps = 6
9. US-08-973-363-10' (1-6608) US-08-973-363-32 Sequence 32, Application US/08973363	5850 5860 5870 5880 5890 5900 5910 ATAGTCAGATTCACTTCTCACAAACTGCTTTATCCCCATCTTC AGAAACCCAGGCTAAGGCACTTACAGACCAAGAACCCGGCTAAGGAGTTACAGACCCGTTGCA 30 40 50 60 70 80 90 5920 5930 5940 5950 5960 5970 X 5980 TGATGACTGACCCCTACCCCTGACATTGCGACTCTCTTATGCT TCATAAAATTACTGATAAAAGACCTTGACAGAAAGAACGACTTGC 100 110 120 130 140 150 X 5990 6000 6010 6020 ATCATCGGCCAGAACCTCTCACTCTGGATGAGTCCTCT 	31 35%保守性Substitutions Gaps = 6
7. US-08-973-363-10' (1-6608) US-08-973-363-3 Sequence 3, Application US/08973363	500 510 520 530 540 550 560 GAGFTGTTGGAAAGGACAGGAAAGAAAAGCTGACGGAAAAGCTGAC ACTCCATCACAGAAAGAACGGCCAAAAGGCTG-----GAGACCTCTCCGAGAAAT 30 40 50 60 70 80 90 500 510 520 530 540 550 560 GAGFTGTTGGAAAGGACAGGAAAGAAAAGCTGACGGAAAAGCTGAC ACTCCATCACAGAAAGAACGGCCAAAAGGCTG-----GAGACCTCTCCGAGAAAT 30 40 50 60 70 80 90	31 35%保守性Substitutions Gaps = 6

